

IN THE SPECIFICATION:

Page 1, line 1, rewrite the title as follows:

- -DNA MOLECULE ENCODING DEF-LIKE MADS-BOX-GENES FROM
PHALAENOPSIS ORCHID- -

Page 1, line 3 before “Background of the Invention”, insert

- -This application claims the benefit of priority under 35 USC 119 of Taiwan
application number 091125320, filed October 25, 2002.- -

Please replace the paragraph beginning on page 5, line 11 with the following:

FIG. 3 illustrates alignment of the consensus sequences for PI-derived motif and
paleoAP3 motif. PeMADS2, PeMADS3, PeMADS4, and PeMADS5 are from *P. equestris*;
OSMADS16 is from rice; SILKY1 is from maize; ~~TPR6~~ DR6 is from *L. esculentum*;
TAMADS51 is from *T. aestivum*; SmAP3 is from *S. montevidensis*; PnAP3-2 is from *P.*
nudicaule; MfAP3 is from *M. figo*; DeAP3 is from *D. eximia*; CMB2 is from *D.*
caryophyllus; LMADS1 is from *L. longiflorum*.

Please replace the paragraph beginning on page 8, line 14 and replace with the following:

As shown in FIG. 3, there is a PI-derived motif (~~FXFRLOPSQPNLH~~)
(FXFRLOPSQPNLH) in PeMADS2, PeMADS3 and PeMADS4 (SEQ ID NO: 25), which is
of more than 60 % homology and a paleoAP3 motif (YGXHDLRLA) (SEQ ID NO: 26).

(Moon, Y.-H. *et al.*, 1999. Identification of a rice *APETALA3* homologue by yeast two-hybrid screening. *Plant Mol. Biol.* 40, 167-177.) However, PeMADS5 shows no significant similarity. Except the Pi-derived motif and paleoAP3 motif, the C-terminal domains of the PeMADS genes have a great variation, which suggests that the four PeMADS genes identified in the EST database indeed exist.

Page 27, after last line, delete the Sequence Listing in entirety and substitute the Sequence Listing attached hereto.